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The Crystal Structure of the Major Dust Mite Allergen Der p 2

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The crystal structure of the common house mite (*Dermatophagoides* sp.) Der p 2 allergen was solved at 2.15 Å resolution using the MAD phasing technique, and refined to an R-factor of 0.209. The refined atomic model, which reveals an immunoglobulin-like tertiary fold, differs in important ways from the previously described NMR structure, because the two beta-sheets are significantly further apart and create an internal cavity, which is occupied by a hydrophobic ligand. This interaction is structurally reminiscent of the binding of a prenyl group by a regulatory protein, the Rho guanine nucleotide exchange inhibitor. The crystal structure suggests that binding of non-polar molecules may be essential to the physiological function of the Der p 2 protein.